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OM protein - protein search, using sw model

Run on: July 8, 2005, 15:22:21 ; Search time 177 Seconds
(without alignments)
167.800 Million cell updates/sec

Title: US-10-617-978-20

Perfect score: 343

Sequence: 1 ADVPGNYPLDSSDNTYLCAPI.....GYCYAFOCWCFLKDENVKV 58

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	222	64.7	58	1 BIRT_PAPR	P58752 parabuthus Q6wJF5
2	188	54.8	80	2 SCXK_CENNO	P63019 centruroides Q6wJF5 mesobuthus
3	127	37.0	67	1 SCXK_CENNO	P56616 centruroides Q6wJY9
4	123	35.9	64	2 Q6V4Y9	P63019 centruroides Q6wJY9
5	119	34.8	65	1 SCXM_CENSC	P6194y8 centruroides Q6wJY8
6	117	34.1	64	2 Q6V4Y8	P01494 centruroides Q6wJY0
7	117	34.1	87	1 SCX2_CENSC	P01494 centruroides Q6wJY0
8	117	34.1	87	1 SCX3_CENSC	P01494 centruroides Q6wJY0
9	116	33.8	64	2 Q6V4Y4	P01494 centruroides Q6wJY4
10	116	33.8	64	2 Q6V4Y4	P01494 centruroides Q6wJY4
11	115	33.5	64	2 Q6V4Y7	P01494 centruroides Q6wJY7
12	115	33.5	73	2 Q68PG2	P01494 centruroides Q6wJY2
13	115	33.5	85	1 Q6V4T3	P01494 centruroides Q6wJY5
14	113	32.9	66	2 Q68PG4	P01494 centruroides Q6wJY4
15	113	32.9	67	2 Q68PG7	P01494 centruroides Q6wJY7
16	113	32.9	87	1 SCXB_CENLL	P45663 centruroides Q6wJY6
17	111	32.4	87	1 SCX5_CENNO	P01490 centruroides Q6wJY6
18	110	32.1	66	1 SCX2_CENSU	P19926 centruroides Q6wJY6
19	110	32.1	87	1 SCB3_CENSC	P01492 centruroides Q6wJY6
20	109	31.8	64	2 Q6V4T3	P01495 centruroides Q6wJY6
21	109	31.8	66	1 SCXR_CENLL	P45667 centruroides Q6wJY6
22	109	31.8	87	1 SCXX_CENNO	P45664 centruroides Q6wJY6
23	109	31.5	66	1 SCX8_CENNO	P01490 centruroides Q6wJY6
24	108	31.5	66	1 SCX2_CENLL	P58898 centruroides Q6wJY6
25	108	31.5	84	1 SCX2_CENNO	P01495 centruroides Q6wJY6
26	107	31.2	64	2 Q6V4Y1	P01491 centruroides Q6wJY6
27	107	31.2	64	2 Q6V4Y2	P01492 centruroides Q6wJY6
28	107	31.2	64	2 Q6V4Y6	P01496 centruroides Q6wJY6
29	107	31.2	66	1 SCX1_CENLI	P58897 centruroides Q6wJY6
30	107	31.2	66	1 SCX1_CENLI	P19926 centruroides Q6wJY6
31	107	31.2	66	1 SCX1_CENLI	P45666 centruroides Q6wJY6

ALIGNMENTS

RESULT 1

BIRT_PAPR STANDARD PRT; 58 AA.

ID BIRT_PAPR
AC P5B752;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DR Bittoxin.
OS Parabuthus transvaalicus (South African fat-tail scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthidae; Buthidae; Butidae; Parabuthus.
RN [1]
RP SEQUNCR.

RC TISSUE=venom; PubMed=11606203;
RX MEDLINE=2151524; PubMed=11606203;
RA Inceoglu B., Lango J., Wu J., Hawkins P., Southern J., Hammock B.D.;
RT "Isolation and characterization of a novel type of neurotoxic peptide from the venom of the South African scorpion Parabuthus transvaalicus (Buthidae)." Buit. J. Biochem. 268:5407-5413 (2001).

-I- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission (By similarity). Moderately toxic, but very high abundant. Lethal to mice. Do not target reptilian channels.

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
DR HSSP: P41964; 1MYN.
DR InterPro; IPR020261; Scorpion_toxin1L.
DR Pfam; PF00537; Toxin_3; 1.
DR ProDom; PD000908; Scorpion_toxin1L.
DR KWR Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
KW KWR Direct protein sequencing; Ionic channel inhibitor; Toxin.
FT DISULFID 18 41 By similarity.
FT DISULFID 18 46 By similarity.
FT DISULFID 27 46 By similarity.
SQ SEQUENCE 58 AA; 658 MW; F5C9EA211959096 CRC64;

Query Match Score 222; DB 1; Length 58;
Best Local Similarity 60.3%; Prod. No. 2-4-18;
Matches 35; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ADVPGNYPLDSSDNTYLCAPI.....GYCYAFOCWCFLKDENVKV 58
Db 1 ADVPGNYPLDSSDNTYLCAPI.....GYCYAFOCWCFLKDENVKV 58

RESULT 2

QWJF5 PRELIMINARY;
ID QWJF5 PRT; 80 AA.
AC QWJF5
DT 05-JUL-2004 (TREMBLref. 27, Created)
DT 05-JUL-2004 (TREMBLref. 27, Last sequence update)